CLAIMS

1. A method for identifying specific characteristics of target polynucleotides present in a sample, comprising the steps of:

i) attaching to one end of each target polynucleotide in the sample a polynucleotide signal sequence that is specific for the characteristic under study;

ii) contacting the target polynucleotides with a molecule that interacts with the target polynucleotide if the characteristic is present;

iii) separating those target polynucleotides that interact from those that do not;

iv) optionally repeating steps (i) to (iii); and

(v) identifying which signal sequences are present on the separated target polynucleotides, and in which order, to thereby determine the characteristics of each target polynucleotide.

2. A method according to claim 1, wherein step (iii) is carried out by

(a) attaching a polynucleotide adapter sequence to those target polynucleotides that interact with the molecule; and

(b) carrying out a polynucleotide amplification reaction on those target polynucleotides that comprise both the signal sequence and adapter.

3. A method according to claim 1 or claim 2, wherein the method is carried out to determine the nucleic acid sequence of the target polynucleotides.

4. A method according to claim 2, wherein the adapter polynucleotide comprises a restriction enzyme recognition sequence that permits later cleavage after the amplification step.

5. A method according to claim 2, wherein amplification is carried out using the polymerase reaction.

6. A method according to claim 5, wherein the adapter and signal sequence comprise recognition sites for oligonucleotide primers used in the polymerase reaction.

7. A method according to any preceding claim, wherein the sample is separated into n reaction compartments, where n is the number of different

characteristics under study, and the signal sequence for each compartment is specific for that compartment.

8. A method according to claim 4, wherein the restriction enzyme recognition sequence is specific for a class IIs enzyme.

9. A method according to claim 8, wherein the enzyme is SfaNI or EarI.

10. A method according to claim 5, wherein the polymerase reaction is carried out using methyl-dCTP as a replacement for dCTP.

11. A method according to claim 2, wherein the adapter is immobilised on a support material.

12. A method according to claim 6, wherein sequential signal sequences and optionally sequential adapters comprise recognition sites for different oligonucleotide primers.

13. A method for determining the sequence of a target polynucleotide, comprising the steps of:

i) treating a sample of a double-stranded target polynucleotide to create overhangs at each end, one of which is to be sequenced, each overhang having a defined number of bases;

ii) dividing the sample and contacting each separate sample with a double-stranded polynucleotide signal sequence and a double stranded adapter polynucleotide, each signal sequence representing a specific polynucleotide sequence of the same length as that of the overhang to be sequenced and comprising an overhang that permits hybridisation and ligation to the end of the target polynucleotide opposite that being sequenced, and each adapter comprising an overhang that is of complementary sequence to the overhang sequence being sequenced;

iii) carrying out the polymerase reaction on the sample(s) using primers that hybridise at the ends of the signal sequence and adapter sequence, wherein the product of the polymerase reaction comprises a restriction site that permits cleavage of the adapter to form a new overhang to be sequenced optionally repeating steps (i) to (iii) using restriction enzymes to create the

overhangs; and

iv) identifying which signal sequences are present on the amplified products, and in which order, to thereby determine the sequence of the target polynucleotide.

14. A method according to claim 13, wherein the overhang that ligates to the signal sequence is at least 3 bases.

15. A method according to claim 13 or claim 14, wherein the overhang to be sequenced is 4 bases.